

# Package ‘CNSimGenome3’

October 15, 2021

**Title** Simulated genome for CN signature validation (#3)

**Description** Simulated genome (#3) for CN signature validation

**Version** 1.0

**Author** The Bioconductor Dev Team

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**Depends** R (>= 3.5.0), BSgenome (>= 1.58.0)

**Imports** BSgenome

**Suggests**

**License** Artistic-2.0

**organism** none

**common\_name** none

**genome** GRCh37

**provider** LM

**release\_date** 2021

**source\_url** none

**biocViews** AnnotationData, Genetics, BSgenome, none

**NeedsCompilation** no

## R topics documented:

CNSimGenome3 . . . . . 1

**Index** 3

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CNSimGenome3	<i>Simulated genome for CN signature validation (#3)</i>
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## Description

Simulated genome (#3) for CN signature validation

**Note**

This BSgenome data package was made from the following source data files:

```
-- information not available --
```

See [?BSgenomeForge](#) and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the **BSgenome** software package for how to make a BSgenome data package.

**Author(s)**

The Bioconductor Dev Team

**See Also**

- [BSgenome](#) objects and the [available.genomes](#) function in the **BSgenome** software package.
- [DNAString](#) objects in the **Biostrings** package.
- The BSgenomeForge vignette (vignette("BSgenomeForge")) in the **BSgenome** software package for how to make a BSgenome data package.

**Examples**

```
CNSimGenome3
genome <- CNSimGenome3
head(seqlengths(genome))

## -----
## Genome-wide motif searching
## -----
## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```

# Index

## \* **data**

CNSimGenome3, [1](#)

## \* **package**

CNSimGenome3, [1](#)

available.genomes, [2](#)

BSgenome, [2](#)

BSgenomeForge, [2](#)

CNSimGenome3, [1](#)

CNSimGenome3-package (CNSimGenome3), [1](#)

DNAString, [2](#)